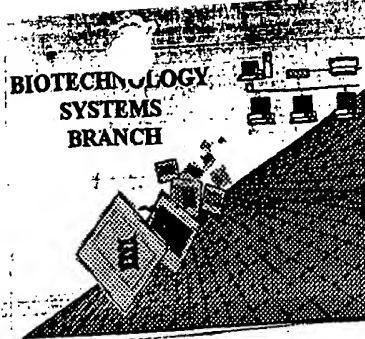


RAW SEQUENCE LISTING ERROR REPORT



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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/383,789A

Source: 1653

Date Processed by STIC: 12/28/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:**

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 08/383789A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

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TECH CENTER 1600/2900
- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
 - 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
 - 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
 - 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
 - 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
 - 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
 - 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
 - 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
 - 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
 - 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
 - 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES) 1-4
 - 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
 - 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/383,789ADATE: 12/28/2000
TIME: 08:06:47Input Set : A:\X-12013.txt
Output Set: N:\CRF3\12282000\I383789A.rawTECH CENTER 10002000
Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Hughes, Benjamin
4 Wolff, Ronald
6 <120> TITLE OF INVENTION: METHOD FOR ADMINISTERING INSULINOTROPIC PEPTIDES
8 <130> FILE REFERENCE: X-12013
10 <140> CURRENT APPLICATION NUMBER: 09/383,789A
11 <141> CURRENT FILING DATE: 1999-08-26
13 <150> PRIOR APPLICATION NUMBER: US 60/098273
14 <151> PRIOR FILING DATE: 1998-08-28
16 <150> PRIOR APPLICATION NUMBER: US 60/100012
17 <151> PRIOR FILING DATE: 1998-09-11
19 <160> NUMBER OF SEQ ID NOS: 4
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 29
25 <212> TYPE: PPT
26 <213> ORGANISM: Artificial/Unknown
28 <220> FEATURE:
29 <221> NAME/KEY: PEPTIDE
30 <222> LOCATION: (1)..(1)
31 <223> OTHER INFORMATION: X at position 1 is Ala, Gly, Val, Thr, Ile and alpha-methyl-Ala.
34 <220> FEATURE:
35 <221> NAME/KEY: PEPTIDE
36 <222> LOCATION: (14)..(14)
37 <223> OTHER INFORMATION: X at position 14 is Glu, Gln, Ala, Thr, Ser and Gly.
40 <220> FEATURE:
41 <221> NAME/KEY: PEPTIDE
42 <222> LOCATION: (20)..(20)
43 <223> OTHER INFORMATION: X at position 20 is Glu, Gln, Ala, Thr, Ser and Gly.
46 <400> SEQUENCE: 1
48 Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Xaa Gly Gln
49 1 5 10 15
51 Ala Ala Lys Xaa Phe Ile Ala Trp Leu Val Lys Gly Arg
52 20 25
54 <210> SEQ ID NO: 2
55 <211> LENGTH: 29
56 <212> TYPE: PPT
57 <213> ORGANISM: Artificial/Unknown
59 <220> FEATURE:
60 <221> NAME/KEY: PEPTIDE
61 <222> LOCATION: (28)..(28)
62 <223> OTHER INFORMATION: X at position 28 is Lys
65 <220> FEATURE:
66 <221> NAME/KEY: PEPTIDE
67 <222> LOCATION: (29)..(29)
68 <223> OTHER INFORMATION: X at position 29 is Gly or is absent
71 <400> SEQUENCE: 2
73 His Ala Glu Gly Phe Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly

Per 1.823 of new sequence rules, the
only valid <213> responses are: Unknown,
Artificial Sequence, or Scientific name
(Genus/species)

one of the
three - do not
combine responses

(see item 12 on
Error Summary
sheet)

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/383,789A

DATE: 12/28/2000
 TIME: 08:06:47

Input Set : A:\X-12013.txt
 Output Set: N:\CRF3\12282000\I383789A.raw

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OK 74 1 5 10 15
 76 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Xaa Xaa
 77 20 25
 79 <210> SEQ ID NO: 3
 80 <211> LENGTH: 29
 81 <212> TYPE: PRK
 82 <213> ORGANISM: Artificial/Unknown
 84 <220> FEATURE:
 85 <221> NAME/KEY: PEPTIDE
 86 <222> LOCATION: (19)..(19)
 87 <223> OTHER INFORMATION: X at position 19 is Lys or Arg.
 90 <400> SEQUENCE: 3
 92 Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln
 93 1 5 10 15
 OK 95 Ala Ala Xaa Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
 96 20 25
 98 <210> SEQ ID NO: 4
 99 <211> LENGTH: 31
 100 <212> TYPE: PRK
 101 <213> ORGANISM: Artificial/Unknown
 103 <220> FEATURE:
 104 <221> NAME/KEY: misc_feature
 105 <222> LOCATION: ()..()
 106 <223> OTHER INFORMATION: Description of Artificial Sequence
 109 <400> SEQUENCE: 4
 111 His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 112 1 5 10 15
 114 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
 115 20 25 30

VERIFICATION SUMMARY

DATE: 12/28/2000

PATIENT APPLICATION: US/09/383,789A

TIME: 08:06:48

Input Set : A:\X-12013.txt

Output Set: N:\CRF3\12282000\I383789A.raw

L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

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